

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.1 [Aug-1-2001]

Matrix gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☐

Sequence 1 lcl|seq_1 Length 510 (1..510)

Sequence 2 lcl|seq_2 Length 512 (1..512)

2

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 786 bits (2029), Expect = 0.0
Identities = 419/522 (80%), Positives = 448/522 (85%), Gaps = 22/522 (4%)

Query: 1 MFIESFRVESPHVRYGAAEIESDYQYDTTEL VHESH DGASRWIVRPKSVRYNFRTTTTVP
60 MFIESFRVESPHVRYGAAEIES+Y+YDTTEL VHESH DGASRW+VRPKSV+Y+FRT+TTVP
Sbjct: 1 MFIESFRVESPHVRYGAAEIESEYRYDTTEL VHESH DGASRWVVRPKSVQYHFRTSTTVP
60

Query: 61 KLGVMLVGWGGNNGSTLTAGVIANREGISWATKDKVQQANYYGSLTQASTIRVGSYN GEE
120 KLGVMLVGWGGNNGSTLTAGVIA+REGISWATKDKVQQANYYGSLTQASTIRVGSYN GEE
Sbjct: 61 KLGVMLVGWGGNNGSTLTAGVIASREGISWATKDKVQQANYYGSLTQASTIRVGSYN GEE
120

Query: 121 IYAPFKSLLPMVNPDDL VFGGWDISNMNLADAMTRAKVLDIDLQQLRPYMES-----
173 IYAPFKSLLPMVNPDDL VFGGWDISNMNLADAMTRAKVLDIDLQQLRPYMES
Sbjct: 121 IYAPFKSLLPMVNPDDL VFGGWDISNMNLADAMTRAKVLDIDLQQLRPYMESWCLSLAS
180

Query: 174 MVPL--PGIYDPDVIAANQGSRRANNVIKGTKKEQMEQIIKDIREFKEKSKVDKVVVLWTA
231 M+P P DP A SR ++ + + KDIREFKE +K+DK VVIWTA
Sbjct: 181 MIPTSSPLTRDP---ARTMSSRE-----PRRSRWGRSSKDIREFKENNMOKAVVILWTA
231

Fig: 1

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Query: 232 NTERYSN-VCVGLNDTMENLLASVDKNEAEISPSTLYAIACV-MEGIPFIINGSPQNTFVP
289

NTERY+N ICIGL T ASVD+NIAEISPSTLY IEG+ I G+ + P
Sbjct: 232 NTERYNNCLCLGLM-TNGKPSASVDRNQAEISPSTLYCHCLASLEGVRSITGALKKKSWP
290

Query: 290 GLIDLAIKNNCLI-GGDDFKSGQTKMKSVLVDFLVGAGIKPTSIVSYNHLGNNDGMNLSA
348

G+ DLAIK GG K G+ K K+ LVDFL+GAGIKPTSIVSYNHLGNNDG NLSA
Sbjct: 291 GIDDLAIKKKLDPGGGLIQKRGKPKKKTGLVDFLMGAGIKPTSIVSYNHLGNNDGTNLSA
350

Query: 349 PQTFRSKEISKSNVDDMVSSNAILYELGEHPDHVVVIKYVPYVGDSKRAMDEYTTSEIFM
408

PQTFRSKEISKS+VVDDMVSSNAILYE GEHPDHVVVIKYVPYVGDSKRAMDEYTTSEIFM
Sbjct: 351 PQTFRSKEISKSSVDDMVSSNAILYEPGEHPDHVVVIKYVPYVGDSKRAMDEYTTSEIFM
410

Query: 409 GKGSTIVLHNTCEDSLAAPIILDVLVLAELSTRIQIKAEGEKFKHSFHPVATILSYLTK
468

GKG+TIVLHNTCEDSLAAPIILDVLVLAELSTRIQLK EGEEKFKHSFHPVATILSYLTK
Sbjct: 411 GKGNTIVLHNTCEDSLAAPIILDVLVLAELSTRIQLKGEGEKFKHSFHPVATILSYLTK
470

Query: 469 APLVPPGTPVVNALAKQRAMLENIMRACVGLAPENNMILEYK 510
APLVPPGTPVVNALAKQRAMLENIMRACVGLAPENNMILEYK

Sbjct: 471 APLVPPGTPVVNALAKQRAMLENIMRACVGLAPENNMILEYK 512

CPU time: 0.10 user secs. 0.02 sys. secs 0.12 total
secs.

Gapped

Lambda	K	H
0.316	0.134	0.385

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 2125

Number of Sequences: 0

Number of extensions: 153

Number of successful extensions: 5

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 510

length of database: 233,319,389

effective HSP length: 125

effective length of query: 385

effective length of database: 176,133,389

effective search space: 67811354765

effective search space used: 67811354765

Fig: 1 (Cont'd)

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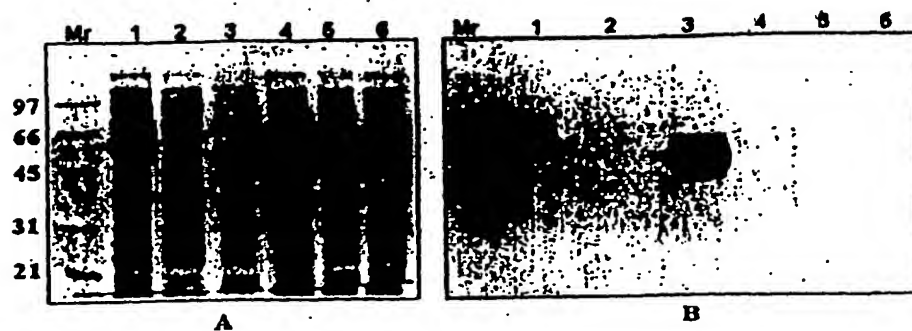


Fig : 2

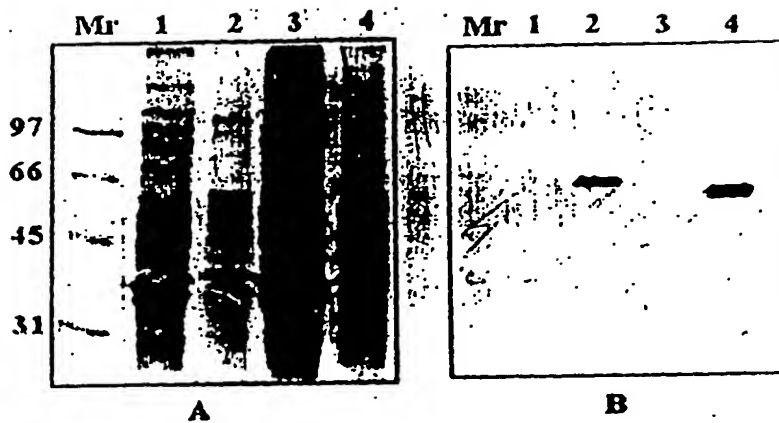


Fig : 3

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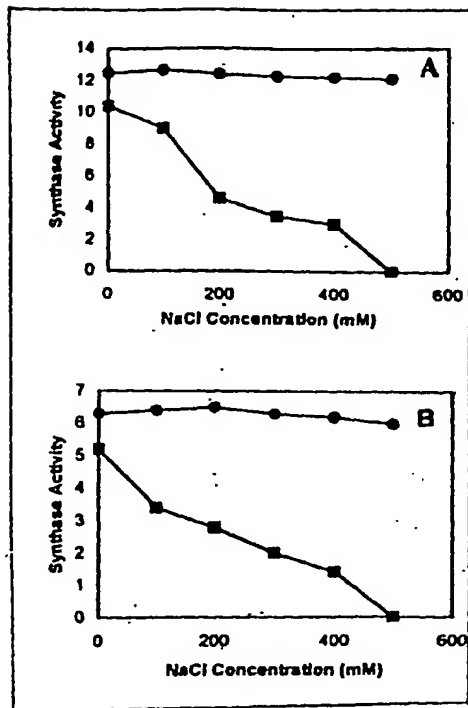


Fig : 4

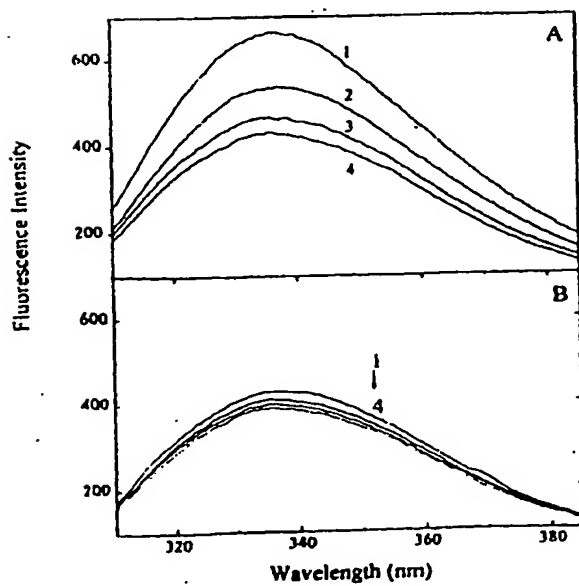


Fig. 5

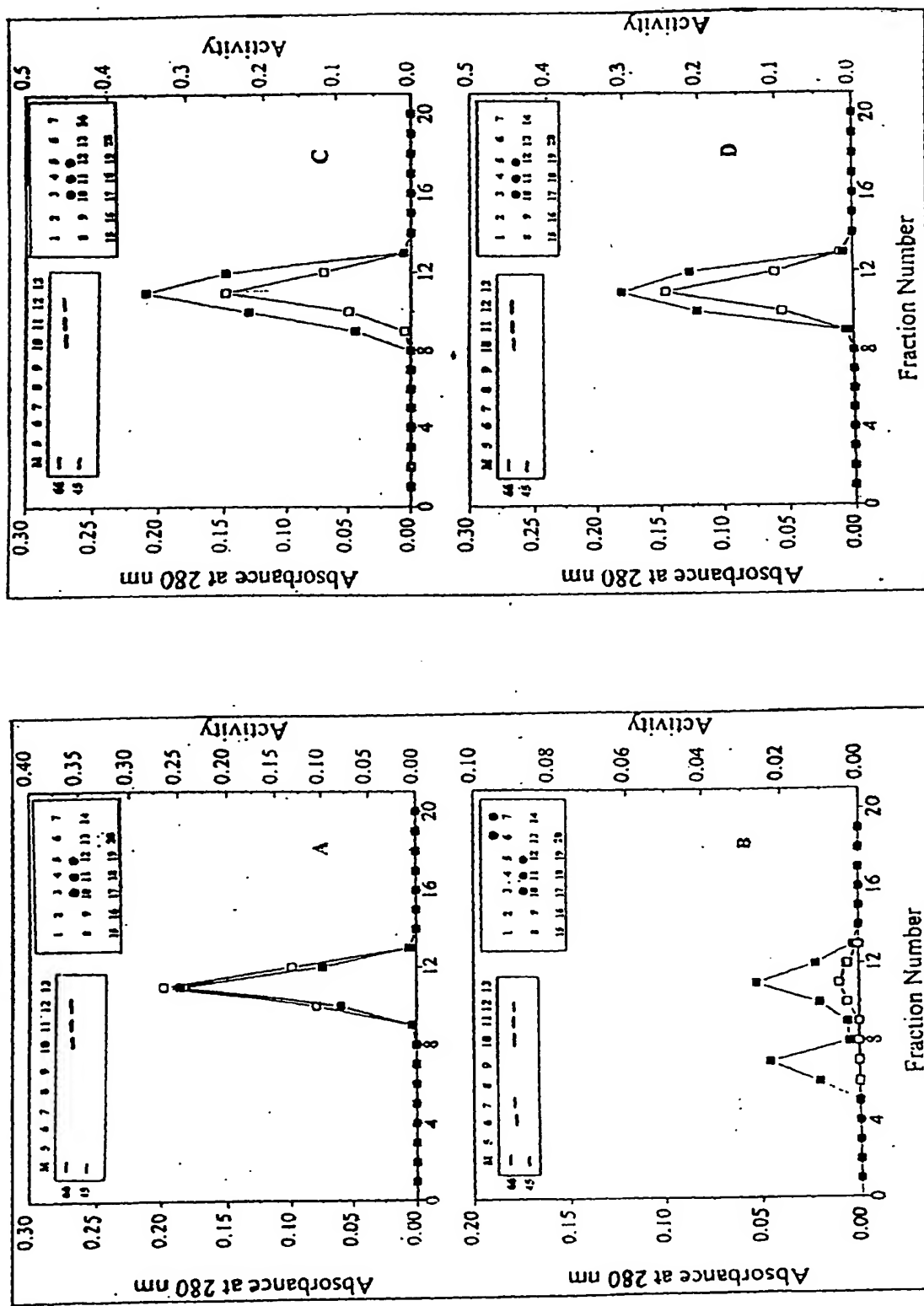


Fig. 6

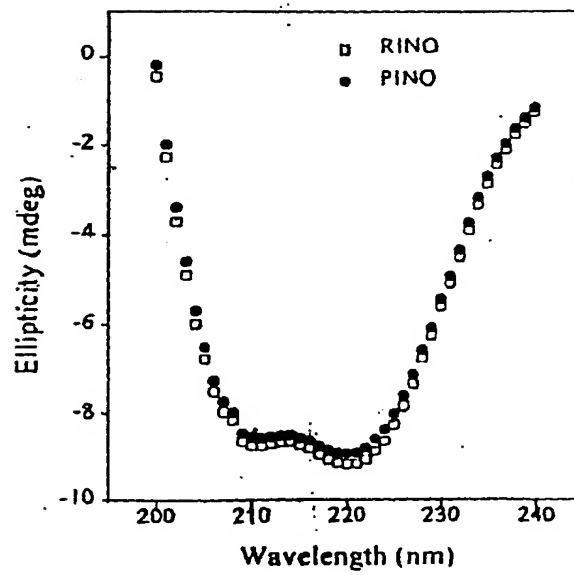


Fig: 7